

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:26:02 ; Search time 12 Seconds  
(without alignments)  
155.522 Million cell updates

Title: US-09-202-035-1

Perfect score:

Sequence: 1 KQRQNKPPSKPNDFHFEVF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

scoring cable. BLOSOM2  
Gapop 10.0 , Gapext 0.5

Searched: 130548 seqs, 38086901 residues

Total number of hits satisfying chosen parameters: 130548

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Processing: Minimum Match 0%  
Maximum Match 100%

Maximum match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1:	/cgn2_6/p/tdata/2/paa/PCT_NEW_COMB pep:*
2:	/cgn2_6/p/tdata/2/paa/US06_NEW_COMB pep:*
3:	/cgn2_6/p/tdata/2/paa/US07_NEW_COMB pep:*
4:	/cgn2_6/p/tdata/2/paa/US08_NEW_COMB pep:*
5:	/cgn2_6/p/tdata/2/paa/US09_NEW_COMB pep:*
6:	/cgn2_6/p/tdata/2/paa/US10_NEW_COMB pep:*
7:	/cgn2_6/p/tdata/2/paa/US60_NEW_COMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	70	24.3	68	5	US-09-513-999C-6913	Sequence 6913, Ap
2	57	19.8	836	5	US-09-724-676-57036	Sequence 57036, A
3	57	19.8	836	5	US-09-724-676-57037	Sequence 57037, A
4	57	19.8	836	5	US-09-724-676-57038	Sequence 57038, A
5	57	19.8	836	5	US-09-724-676-57039	Sequence 57039, A
6	57	19.8	836	5	US-09-724-676-57040	Sequence 57040, A
7	57	19.8	836	5	US-09-724-676-57041	Sequence 57041, A
8	57	19.8	836	5	US-09-724-676-57071	Sequence 57071, A
9	57	19.8	836	5	US-09-724-676-57072	Sequence 57072, A
10	57	19.8	836	5	US-09-724-676-57073	Sequence 57073, A
11	57	19.8	836	5	US-09-724-676-57074	Sequence 57074, A
12	57	19.8	836	5	US-09-724-676-57075	Sequence 57075, A
13	57	19.8	836	5	US-09-724-676-57077	Sequence 57077, A
14	57	19.8	836	5	US-09-724-676-57108	Sequence 57108, A
15	57	19.8	836	5	US-09-724-676-57110	Sequence 57110, A
16	57	19.8	836	5	US-09-724-676-57111	Sequence 57111, A
17	57	19.8	836	5	US-09-724-676-57112	Sequence 57112, A
18	57	19.8	836	5	US-09-724-676-57113	Sequence 57113, A
19	57	19.8	836	5	US-09-724-676-57114	Sequence 57114, A
20	55	19.1	165	5	US-09-513-999C-7900	Sequence 7900, Ap
21	54	18.8	142	5	US-09-724-676-83811	Sequence 83811, A
22	54	18.8	142	5	US-09-724-676-83813	Sequence 83813, A
23	52	18.1	69	1	PCT-US02-32727-57376	Sequence 27376, A
24	51.5	17.9	216	5	US-09-724-676-53566	Sequence 53566, A
25	51.5	17.9	270	5	US-09-724-676-53564	Sequence 53564, A
26	51.5	17.9	270	5	US-09-724-676-53565	Sequence 53565, A

## ALIGNMENTS

## RESULT 1

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US-09-513-999C-6913
; Sequence 6913, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.052.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6913
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6913

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Query Match      24.3%; Score 70; DB 5; Length 68;
Best Local Similarity 29.6%; Pred. No. 0.098;
Matches 16; Conservative 6; Mismatches 12; Indels 20; Gaps 3;

QY  7  PPSKPNNDHFVEVNF-----VPC-----SICSNRPCTCAICKRIP 42
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Db  3  PPQR--NSFFFIYLYLNNRDEVSPCCGWCQSPGLKQSGICPGSPKWDYCRKPP 54
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## RESULT 2

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US-09-724-676-57036
; Sequence 57036, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57036
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57036

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Query Match 19.8%; Score 57; DB 5; Length 836;  
Best Local Similarity 32.4%; Pred. No. 23;



<pre>; NUMBER OF SEQ ID NOS: 97222 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 57071 ; LENGTH: 836 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-57071</pre>	<pre>Query Match      19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;</pre>
<pre>QY   3 RQNKPPSKPNNDHFHFEVFNFPVCISCSNNPTCWA 36       :    : :     :   :        Db   794 RSEAPSWEQHCWRTGGTGGFVCCCLCIQGPGVCWA 827</pre>	
RESULT 9	
<pre>US-09-724-676-57072 ; Sequence 57072, Application US/09724676 ; GENERAL INFORMATION: ; APPLICANT: Compugen LTD ; TITLE OF INVENTION: Variants of alternative splicing ; FILE REFERENCE: 129181.4 CompuGen ; CURRENT APPLICATION NUMBER: US/09/724,676 ; CURRENT FILING DATE: 2000-11-28 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 57072 ; LENGTH: 836 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-57072</pre>	<pre>Query Match      19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;</pre>
<pre>QY   3 RQNKPPSKPNNDHFHFEVFNFPVCISCSNNPTCWA 36       :    : :     :   :        Db   794 RSEAPSWEQHCWRTGGTGGFVCCCLCIQGPGVCWA 827</pre>	
RESULT 10	
<pre>US-09-724-676-57073 ; Sequence 57073, Application US/09724676 ; GENERAL INFORMATION: ; APPLICANT: Compugen LTD ; TITLE OF INVENTION: Variants of alternative splicing ; FILE REFERENCE: 129181.4 CompuGen ; CURRENT APPLICATION NUMBER: US/09/724,676 ; CURRENT FILING DATE: 2000-11-28 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 57073 ; LENGTH: 836 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-57073</pre>	<pre>Query Match      19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;</pre>
<pre>QY   3 RQNKPPSKPNNDHFHFEVFNFPVCISCSNNPTCWA 36       :    : :     :   :        Db   794 RSEAPSWEQHCWRTGGTGGFVCCCLCIQGPGVCWA 827</pre>	
RESULT 11	
<pre>US-09-724-676-57074 ; Sequence 57074, Application US/09724676 ; GENERAL INFORMATION:</pre>	<pre>Query Match      19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;</pre>
<pre>QY   3 RQNKPPSKPNNDHFHFEVFNFPVCISCSNNPTCWA 36       :    : :     :   :        Db   794 RSEAPSWEQHCWRTGGTGGFVCCCLCIQGPGVCWA 827</pre>	
RESULT 12	
<pre>US-09-724-676-57075 ; Sequence 57075, Application US/09724676 ; GENERAL INFORMATION: ; APPLICANT: Compugen LTD ; TITLE OF INVENTION: Variants of alternative splicing ; FILE REFERENCE: 129181.4 CompuGen ; CURRENT APPLICATION NUMBER: US/09/724,676 ; CURRENT FILING DATE: 2000-11-28 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 57075 ; LENGTH: 836 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-57075</pre>	<pre>Query Match      19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;</pre>
<pre>QY   3 RQNKPPSKPNNDHFHFEVFNFPVCISCSNNPTCWA 36       :    : :     :   :        Db   794 RSEAPSWEQHCWRTGGTGGFVCCCLCIQGPGVCWA 827</pre>	
RESULT 13	
<pre>US-09-724-676-57077 ; Sequence 57077, Application US/09724676 ; GENERAL INFORMATION: ; APPLICANT: Compugen LTD ; TITLE OF INVENTION: Variants of alternative splicing ; FILE REFERENCE: 129181.4 CompuGen ; CURRENT APPLICATION NUMBER: US/09/724,676 ; CURRENT FILING DATE: 2000-11-28 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 57077 ; LENGTH: 836 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-57077</pre>	<pre>Query Match      19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;</pre>
<pre>QY   3 RQNKPPSKPNNDHFHFEVFNFPVCISCSNNPTCWA 36       :    : :     :   :        Db   794 RSEAPSWEQHCWRTGGTGGFVCCCLCIQGPGVCWA 827</pre>	

RESULT 14

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US-09-724-676-57108
; Sequence 57108, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ-ID NO 57108
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57108

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Query Match 19.8%; Score 57; DB 5; Length 836;  
Best Local Similarity 32.4%; Pred. No. 23;  
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 3 RQNKPPSKPNNDFHFEVFNFPVCSICSNNPTCWA 36  
| \_ : || : : || | : | | | |  
Db 794 RSEAPSWEOHCWRTGEGGFVCCCLCIOGPVCWA 827

RESULT. 15

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US-09-724-676-57110
; Sequence 57110, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57110
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-57110

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Query Match 19.8%; Score 57; DB 5; Length 836;  
Best Local Similarity 32.4%; Pred. No. 23;  
Matches 11; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

**Qy** | 3 RQNKPPSKPNNDFHFVEVNFVPCISNNTCWA 36  
| - : || : : || - : ||  
**Db** 794 RSEAPSWEOHCWRTGEGGFVCCCLCTGGPVCA 827

Search completed: November 22, 2002, 14:30:05  
Job time : 12 secs

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	288	100.0	49	16	US-09-202-035-1		Sequence 1, Appl
2	288	100.0	49	16	US-09-202-035-32		Sequence 32, Appl
3	288	100.0	49	16	US-09-202-035-36		Sequence 36, Appl
4	288	100.0	49	16	US-09-202-035-40		Sequence 40, Appl
5	288	100.0	49	16	US-09-202-035-42		Sequence 42, Appl
6	288	100.0	49	16	US-09-202-035-43		Sequence 43, Appl

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RESULT 2
US-09-202-035-32
; Sequence 32, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT FILING DATE: 1998-12-17
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-32
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 3
US-09-202-035-36
; Sequence 36, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT FILING DATE: 1998-12-17
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: acetylation
US-09-202-035-36
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 4
US-09-202-035-38
; Sequence 38, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT FILING DATE: 1998-12-17
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: amidation
US-09-202-035-38
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
RESULT 5
US-09-202-035-42
; Sequence 42, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT FILING DATE: 1998-12-17
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: benzoyl benzylamide derivatisation
US-09-202-035-42
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-202-035-40
; Sequence 40, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT FILING DATE: 1998-12-17
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: fluorescein isothiocarbamyl beta-alanine
; OTHER INFORMATION: derivatisation
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: amidation
US-09-202-035-40
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
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RESULT 5
US-09-202-035-42
; Sequence 42, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT FILING DATE: 1998-12-17
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: benzoyl benzylamide derivatisation
US-09-202-035-42
Query Match 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
Db 1 KORQKPPSKPNDFHFVFNVPSCSNNPTCWAICKRIPNKKPGKK 49
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Query Match      100.0%; Score 288; DB 27; Length 298;
Best Local Similarity 100.0%; Pred. NO. 6.1e-25;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KQRONKPPSKPNNDHFHFEVNFVPCISCSNPTCWAICKRIPNKKPGKK 49  
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Db 149 KQRONKPPSKPNNDHFHFEVNFVPCISCSNAPT CWAICKRIPNKKPGKK 197  
|||||

RESULT 8

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US-09-202-035-2
; Sequence 2, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-2

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 2.3e-25;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKNNDFHFEVFNVPSCISGNNPTCWAICKRIPNKKPGKK 49
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Db 1 KORQNKPPSKNNDFHFEVFNVPSCISGNNPTCWAICKRIPNKKPGKK 49
      |||||

RESULT 9
US-09-202-035-3
; Sequence 3, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-3

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 2.3e-25;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKNNDFHFEVFNVPSCISGNNPTCWAICKRIPNKKPGKK 49
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Db 1 KORQNKPPSKNNDFHFEVFNVPSCISGNNPTCWAICKRIPNKKPGKR 49
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RESULT 10
US-09-202-035-5
; Sequence 5, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04

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US-09-202-035-5

US 09-202-035-8  
; Sequence 8, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman

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, TITLE OF INVENTION: Viral replicases with structural homology to protein G
,
, TITLE OF INVENTION: Respiratory Syncytial Virus
,
, FILE REFERENCE: 41582000100
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, CURRENT APPLICATION NUMBER: US/09/202_035

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? EARLIER APPLICATION NUMBER: PC1/A057700351
? EARLIER FILING DATE: 1997-06-04
? EARLIER APPLICATION NUMBER: AU PO 0265
? EARLIER FILING DATE: 1996-06-05
? NUMBER OF SEQ ID NOS: 44
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 8
? LENGTH: 49
? TYPE: prt
? ORGANISM: respiratory syncytial virus
? US-09-202-035-8

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US-03-647-309A-40
? Sequence 40, Application US/09647309A
? GENERAL INFORMATION:
? APPLICANT: Pierre Fabre Medicament
? TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
? FILE REFERENCE: D17064
? CURRENT APPLICATION NUMBER: US/09/647, 309A
? CURRENT FILING DATE: 2002-02-28
?

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? PRIOR FILING DATE: 1998-03-27
?
? NUMBER OF SEQ ID NOS: 136
?
? SOFTWARE: PatentIn Vers. 2.0
?
? SEQ ID NO 40
?
? LENGTH: 59
?
? TYPE: PRT
?
? ORGANISM: Respiratory syncytial Virus (RSV)
? US-09-647-309A-40

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APPLICANT: Pierre Fabre Medicament  
TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY



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; FILE REFERENCE: D17064
; CURRENT APPLICATION NUMBER: US/09/647,309A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: FR 98 03814
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 38
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Respiratory syncytial Virus (RSV)
US-09-647-309A-38
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Query Match      99.0%; Score 285; DB 20; Length 61;
Best Local Similarity 98.0%; Pred. No. 2.9e-25;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KORQNKPPSKPNDFHFVFVPCISCSNNPTCWAICKRIPIKPKGKK 49
Db      10 KORQNKPPKNDFHFVFVPCISCSNNPTCWAICKRIPIKPKGKK 58
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Search completed: November 22, 2002, 14:29:48  
Job time : 142 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 14:24:42 ; Search time 18 Seconds  
(without alignments)  
261.699 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KQRQKPPSKPNDFHFEV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	288	100.0	298	1	MGNZ
2	285	99.0	297	2	major surface glycoprotein G - human respiratory syncytial virus
3	285	99.0	297	2	attachment protein
4	285	99.0	297	2	attachment protein
5	285	99.0	298	1	MGNZKL
6	285	99.0	298	2	major surface glycoprotein G - Human
7	280	97.2	298	2	attachment protein
8	279	96.9	297	2	attachment protein
9	273	94.8	297	2	attachment protein
10	190	66.0	292	1	MGNZ18
11	190	66.0	292	1	major surface glycoprotein G - o
12	83.5	29.0	257	1	MGNZ60
13	80	27.8	263	2	major surface glycoprotein G - b
14	79	27.4	250	2	glycoprotein G - b
15	77.5	26.9	248	2	glycoprotein G - b
16	77.5	26.9	263	2	glycoprotein G - o
17	77.5	26.9	263	2	attachment glycoprotein G - o
18	66.5	23.1	274	2	attachment glycoprotein G - o
19	66.5	23.1	274	2	diaminopimelate ep
20	66.5	23.1	275	1	AC0919
21	66.5	23.1	275	1	S01913
22	66.5	23.1	275	2	C91221
23	64	22.0	37	2	F86067
24	63.5	22.0	274	2	charybdotoxin 2 -
25	63	21.9	1861	2	diaminopimelate ep
26	62	21.5	37	2	microtubule-associ
27	62	21.5	290	2	charybdotoxin 1 [v
28	61	21.2	375	2	diaminopimelate ep
29	60.5	21.0	1506	2	A/G-specific adeni
					hypothetical prote

30 59 20.5 57 2 S70473  
31 58.5 20.3 276 2 G82986  
32 57.5 20.0 276 2 T10459  
33 57.5 20.0 518 2 T25507  
34 57.5 20.0 776 2 T02584  
35 57 19.8 279 2 C70458  
36 57 19.8 532 2 G84775  
37 57 19.8 792 2 A71822  
38 57 19.8 1188 2 S48861  
39 56.5 19.6 117 2 T08663  
40 56.5 19.6 748 2 B45046  
41 55.5 19.3 235 2 I50610  
42 55.5 19.3 747 2 S01918  
43 55 19.1 266 2 B82713  
44 54.5 18.9 902 2 S49931  
45 54 18.8 160 2 B84947

ALIGNMENTS

RESULT 1

MGNZ

major surface glycoprotein G - human respiratory syncytial virus

C:Species: human respiratory syncytial virus

C:Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 24-Sep-1999

C:Accession: A94048; A93599; A04039

R:Wertz, G.W.; Collins, P.T.; Huang, X.; Gruber, C.; Levine, S.; Ball, L.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985

A:Title: Nucleotide sequence of the G protein gene of human respiratory syncytial vlr

A:Reference number: A94048; MUID:85216636; PMID:3858865

A:Accession: A94048

A:Molecule type: mRNA

A:Residues: 1-298 <WER>

A:Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217;

7.1; PID:g333932

A:Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid prot

A:Note: this protein may carry 40-80 separate O-linked carbohydrate chains distribute

R:Satake, M.; Colligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.

Nucleic Acids Res. 13, 7795-7812, 1985

A:Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.

A:Reference number: A93599; MUID:86067198; PMID:406997

A:Accession: A93599

A:Molecule type: mRNA

A:Residues: 1-298 <SAT>

A:Cross-references: GB:X03149; NID:g60997; PID:CAA26928.1; PID:g60998

C:Superfamily: respiratory syncytial virus major surface glycoprotein G

C:Keywords: glycoprotein; transmembrane protein

F:38-66/Domain: transmembrane #status predicted <TNM>

F:85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 288; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.7e-26;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy .1 KQRQKPPSKPNDFHFEVFNFCSTCSNNPTCWAICKRIPNKKPGKK 49

|||||

Db 149 KQRQKPPSKPNDFHFEVFNFCSTCSNNPTCWAICKRIPNKKPGKK 197

RESULT 2

JQ1205

attachment protein - human respiratory syncytial virus (strain RSB1734)

N:Alternate names: G protein

C:Species: human respiratory syncytial virus

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997

C:Accession: JQ1205

R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.

J. Gen. Virol. 72, 2091-2096, 1991

A:Title: Identification of variable domains of the attachment (G) protein of subgroup

A:Reference number: JQ1204; MUID:91374005; PMID:1895054

A:Accession: JQ1205

A:Molecule type: mRNA

RESULT 5

MGNZRL

major surface glycoprotein G - human respiratory syncytial virus (strain Long)

C:Species: human respiratory syncytial virus

C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999

C:Accession: A32703; SI2279

R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.

Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987

A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and B

A:Reference number: A32703; MUID:87289657; PMID:2441388

A:Accession: A32703

A:Molecule type: mRNA

A:Residues: 1-298 <JOH>

A:Cross-references: GB:M17212; NID:G333940; PIDN:AAA47411.1; PID:G333941

R:Garcia-Barteno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.

EMBO J. 9, 4181-4187, 1990

A:Title: Frame shift mutations as a novel mechanism for the generation of neutralizing epitopes in human respiratory syncytial virus

A:Reference number: SI2279; MUID:91065351; PMID:2249671

A:Accession: SI2279

A:Molecule type: mRNA

A:Residues: 1-298 <GAR>

C:Superfamily: respiratory syncytial virus major surface glycoprotein G

C:Keywords: glycoprotein; transmembrane protein

F:41-63/Domain: transmembrane #status predicted <TMM>

F:85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #std

Query Match 99.0%; Score 285; DB 1; Length 298;

Best Local Similarity 98.0%; Pred. No. 3.9e+26;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQRQKPPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPGKK 49

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 149 KQRQKPPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPGKK 197

RESULT 6

JC5680

G protein - Human respiratory syncytial virus

C:Species: Human respiratory syncytial virus

C:Date: 11-Nov-1997 #sequence\_revision 11-Nov-1997 #text\_change 26-Feb-1998

C:Accession: JC5680

R:Geng, X.; Wang, Z.; Qian, Y.; Zhu, R.; Deng, J.; Du, J.; Zhu, Z.

Chinese J. Virol. 12, 317-322, 1996

A:Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain

A:Reference number: JC5680

A:Accession: JC5680

A:Molecule type: mRNA

A:Residues: 1-298 <GEN>

A:Experimental source: strain B79

A:Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for

C:Superfamily: respiratory syncytial virus major surface glycoprotein G

F:1-38/Domain: intracellular #status predicted <INT>

F:39-66/Domain: transmembrane #status predicted <TMM>

F:67-298/Domain: extracellular #status predicted <EXC>

Query Match 99.0%; Score 285; DB 2; Length 298;

Best Local Similarity 98.0%; Pred. No. 3.9e+26;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQRQKPPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPGKK 49

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 149 KQRQKPPKPNDFHFEVFNVPSCISNNPTCWAICKRIPNKKPGKK 197

RESULT 7

JQ1207

attachment protein - human respiratory syncytial virus (strain RSB6190)

N:Alternate names: G protein

C:Species: human respiratory syncytial virus

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997

C:Accession: JQ1207

R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.

```

Matches      46;   Conservative      1;   Mismatches      2;   Indels      0;   Gaps      0;

QY    1 KQRONKPPSPNNDHFHEVFNFVPCSSNNPTCWAICKRIPNKKPGKK 49
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     149 KQHONKPPNPNNHFEVFNFVPCSSNNPTCWAICKRIPNKKPGKK 197

RESULT 10
MGNZ18
major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: B32703
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and
A:Reference number: A32703; MUID:87289657; PMID:2441388
A:Accession: B32703
A:Molecule type: mRNA
A:Residues: 1-292 <OJ>
A:Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TM>
F:81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          66.0%; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred.No. 5.7e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY    1 KQRONKPPSPNNDHFHEVFNFVPCSSNNPTCWAICKRIPNKKPGKK 49
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     149 KSRSKNPKPKDDYHFEVFNFVPCSGCNQLCKSICKTIPS NKPKKK 197

RESULT 11
MGNZ60
major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N:Alternate names: attachment glycoprotein G
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: A37077
R:Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A:Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis
gous subgroup virus challenge.
A:Reference number: A37077; MUID:90357765; PMID:1697126
A:Accession: A37077
A:Molecule type: mRNA
A:Residues: 1-292 <SL>
A:Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945
C:Genetics:
A:Gene: G
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:45-63/Domain: transmembrane #status predicted <TM>
F:81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          66.0%; Score 190; DB 1; Length 292;
Best Local Similarity 65.3%; Pred.No. 5.7e-15;
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY    1 KQRONKPPSPNNDHFHEVFNFVPCSSNNPTCWAICKRIPNKKPGKK 49
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     149 KSRSKNPKPKDDYHFEVFNFVPCSGCNQLCKSICKTIPS NKPKKK 197

RESULT 12
MGNZBR
major surface glycoprotein G - bovine respiratory syncytial virus (strain 391-2)
N:Alternate names: attachment glycoprotein G
C:Species: bovine respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

```

C;Accession: A36408  
J;erch, R.A.; Anderson, K.; Wertz, G.W.  
J. Virol. 64, 5559-5565, 1990  
A;Title: Nucleotide sequence analysis and expression from recombinant vectors demonstrated in syncytial virus.  
A;Reference number: A36408; MUID:91012801; PMID:2214024  
A;Accession: A36408  
A;Molecule type: mRNA  
A;Residues: 1-257 <LER>  
A;Cross-references: GB:M58307; NID:g210830; PIDN:AAA42810.1; PID:g210831  
C;Genetics:  
A;Gene: G  
C;Superfamily: respiratory syncytial virus major surface glycoprotein G  
C;Keywords: glycoprotein; transmembrane protein  
F;45-62/Domain: transmembrane #status predicted <TMN>  
F;3,85,127,149,233,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.0%; Score 83.5; DB 1; Length 257;  
Best Local Similarity 29.6%; Pred. No. 0.017;  
Matches 16; Conservative 9; Mismatches 16; Indels 13; Gaps 2;

QY | 6 KPSPKPNNDP-----HFEVFNVPVPCSGSNNPTCWAIC----KRIPNKKP 46  
| | | | | : : : : | | | | | : : : : | | : : |  
Db | 145 KPINSGSIPPENHQDHNNSQTLPPVPCSTCEGNLACLSLCHIEIETAPSRAP 198

RESULT 13  
JQ2284  
glycoprotein G - bovine respiratory syncytial virus (isolate A51908)  
C;Species: bovine respiratory syncytial virus  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C;Accession: JQ2284  
R;Mallipeddi, S.K.; Samal, S.K.  
J. Gen. Virol. 74, 2001-2004, 1993  
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial virus  
A;Reference number: JQ2284; MUID:93389461; PMID:8376974  
A;Accession: JQ2284  
A;Molecule type: mRNA  
A;Residues: 1-263 <NAL>  
A;Experimental source: isolate A51908  
C;Superfamily: respiratory syncytial virus major surface glycoprotein G  
C;Keywords: glycoprotein; transmembrane protein  
F;1-38/Domain: intracellular #status predicted <INT>  
F;39-66/Domain: transmembrane #status predicted <TMM>  
F;67-263/Domain: extracellular #status predicted <EXT>  
F;127,163,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.8%; Score 80; DB 2; Length 263;  
Best Local Similarity 29.8%; Pred. No. 0.044;  
Matches 14; Conservative 9; Mismatches 20; Indels 4; Gaps 1;

QY | 4 QNKPPSKPNNDPHEVFNVPVPCSGSNNPTCWAIC----KRIPNKKP 46  
| | | | | : : : : | | | | | : : : : | | : : |  
Db | 152 ESNPPENHQDHNNSQTLPPVPCSTCEGNPACSPICQIGLERAPSRAP 198

RESULT 14  
PQ0768  
glycoprotein G - bovine respiratory syncytial virus (isolate FS-1) (fragment)  
C;Species: bovine respiratory syncytial virus  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C;Accession: PQ0768  
R;Mallipeddi, S.K.; Samal, S.K.  
J. Gen. Virol. 74, 2001-2004, 1993  
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial virus  
A;Reference number: JQ2284; MUID:93389461; PMID:8376974  
A;Accession: PQ0768  
A;Molecule type: mRNA  
A;Residues: 1-250 <NAL>  
C;Superfamily: respiratory syncytial virus major surface glycoprotein G  
C;Keywords: glycoprotein; transmembrane protein  
F;1-31/Domain: intracellular #status predicted <INT>  
F;32-59/Domain: transmembrane #status predicted <TMM>

F;60-250/Domain: extracellular #status predicted <EXT>  
F;78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.4%; Score 79; DB 2; Length 250;  
Best Local Similarity 26.7%; Pred. No. 0.055;  
Matches 12; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY | 4 QNKPPSKPNNDPHEVFNVPVPCSGSNNPTCWAICRIPNKKPGK 48  
| | | | | : : : : | | | | | : : : : | | : : |  
Db | 145 ESNPPENHQDHNNSQTLPPVPCSTCEGNLACLSLCQVGPGRAPSR 189

RESULT 15  
PQ0769  
glycoprotein G - bovine respiratory syncytial virus (isolate VC464) (fragment)  
C;Species: bovine respiratory syncytial virus  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
C;Accession: PQ0769  
R;Mallipeddi, S.K.; Samal, S.K.  
J. Gen. Virol. 74, 2001-2004, 1993  
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial virus  
A;Reference number: JQ2284; MUID:93389461; PMID:8376974  
A;Accession: PQ0769  
A;Molecule type: mRNA  
A;Residues: 1-248 <NAL>  
A;Experimental source: isolate VC464  
A;Note: the authors translated the codon ACC for residue 85 as His and ATC for residue 86  
C;Superfamily: respiratory syncytial virus major surface glycoprotein G  
C;Keywords: glycoprotein; transmembrane protein  
F;1-29/Domain: intracellular #status predicted <INT>  
F;30-57/Domain: transmembrane #status predicted <TMM>  
F;58-248/Domain: extracellular #status predicted <EXT>  
F;76,154,224,242/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.9%; Score 77.5; DB 2; Length 248;  
Best Local Similarity 30.8%; Pred. No. 0.081;  
Matches 16; Conservative 8; Mismatches 19; Indels 9; Gaps 2;

QY | 6 KPSPKPNNDP-----NNDFH--FEVFNVPVPCSGSNNPTCWAICRIPNKKPGK 48  
| | | | | : : : : | | | | | : : : : | | : : |  
Db | 136 KPINSGSNPPENHQDHNNSQTLPPVPCSTCEGNLACLSLCQIGPERAPSR 187

Search completed: November 22, 2002, 14:26:59  
Job time : 19 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 14:17:16 ; Search time 11 Seconds  
(without alignments)  
184.758 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KQRNKPSPKPNDFHFVEF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	288	100.0	298	1	VGLG_HRSVA	P03423	human respi
2	285	99.0	297	1	VGLG_HRSV2	P27021	human respi
3	285	99.0	297	1	VGLG_HRSV3	P27022	human respi
4	285	99.0	297	1	VGLG_HRSV6	P27025	human respi
5	285	99.0	298	1	VGLG_HRSVL	P20895	human respi
6	280	97.2	298	1	VGLG_HRSV5	P27024	human respi
7	279	96.9	297	1	VGLG_HRSV4	P27023	human respi
8	273	94.8	297	1	VGLG_HRSV7	P27026	human respi
9	190	66.0	292	1	VGLG_HRSV1	P20896	human respi
10	190	66.0	292	1	VGLG_HRSV8	P23041	human respi
11	83.5	29.0	257	1	VGLG_BRSSVC	P22261	bovine resp
12	80	27.8	263	1	VGLG_BRSSV2	O10685	bovine resp
13	77.5	26.9	257	1	VGLG_BRSSVS	O10686	bovine resp
14	77.5	26.9	263	1	VGLG_BRSSVW	O10687	bovine resp
15	77.5	26.9	263	1	VGLG_ORSSVW	O86695	ovine respi
16	76.5	26.6	263	1	VGLG_BRSSV1	O10683	bovine respi
17	76.5	26.6	263	1	VGLG_BRSSV4	O10684	bovine respi
18	74	25.7	257	1	VGLG_BRSSV	O09495	bovine respi
19	74	25.7	257	1	VGLG_BRSSVR	Q84183	bovine respi
20	73	25.3	257	1	VGLG_BRSSV7	Q5706	bovine respi
21	67.5	23.4	274	1	DAPE_PASMU	P57962	pasteurella
22	66.5	23.1	274	1	DAPE_ECO57	Q8x8p8	escherichia
23	66.5	23.1	274	1	DAPE_ECOLI	P08885	escherichia
24	66.5	23.1	274	1	DAPE_SALTY	Q91606	salmonella
25	66.5	23.1	274	1	DAPE_YERPE	P46357	yersinia pe
26	64	22.2	37	1	SKCK2_LEIQH	P45628	leirus qui
27	63.5	22.0	274	1	DAPE_HAEIN	P44859	haemophilus
28	62	21.5	37	1	SKCK2_LEIQH	P13487	leirus qui
29	62	21.5	276	1	DAPE_VIBCH	Q9kvl6	vibrio chol
30	60.5	21.0	57	1	SKCK1_MESMA	Q9ni16	mesobuthus
31	58.5	20.3	276	1	DAPE_PSEAE	Q31564	pseudomonas
32	57.5	20.0	276	1	DAPE_PSEFL	O05322	pseudomonas
33	57	19.8	279	1	DAPE_AQUAE	O67693	aquifex ae

RESULT 1  
VGLG\_HRSVA STANDARD; PRT; 298 AA.  
AC P03423;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-JUL-1998 (Rel. 36, Last annotation update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (strain A2).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11259;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85216636; PubMed=3858865;  
RA Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;  
RT "Nucleotide sequence of the G protein gene of human respiratory  
RT syncytial virus reveals an unusual type of viral membrane protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86067198; PubMed=4069997;  
RA Satake M., Coligan J.E., Elango N., Norby E., Venkatesan S.;  
RT "Respiratory syncytial virus envelope glycoprotein (G) has a novel  
RT structure.";  
RN [3]  
RP Nucleic Acids Res. 13:7795-7812(1985).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95266253; PubMed=7747420;  
RA Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;  
RT "A cold-passaged, attenuated strain of human respiratory  
RT virus contains mutations in the F and L genes.";  
RL Virology 208:478-484(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97187925; PubMed=9035372;  
RA Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,  
RA Murphy B.R.;  
RT "Acquisition of the ts phenotype by a chemically-mutagenized cold-  
RT passaged human respiratory syncytial virus vaccine candidate results  
RT from the acquisition of a single mutation in the polymerase (L)  
RT gene.";  
RL Virus Genes 13:269-273(1996).  
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
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Q06342 trichoplusi  
P09179 bombyx mori  
P56219 titiys serr  
Q9ni15 mesobuthus  
P40528 saccharomyc  
Q9kvl1 haemophilus  
P57248 buchnera ap  
P97436 mus musculus  
P57649 buchnera ap  
P34878 lactococcus  
P11332 european el  
P25118 mus musculus

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DR EMBL; M11486; AAB59857.1; -  
DR EMBL; X03149; CAA26928.1; -  
DR EMBL; U50362; AAB86663.1; -  
DR EMBL; U50363; AAB86675.1; -  
DR EMBL; U63644; AAC55969.1; -  
DR PIR; A04039; MGZ.  
DR InterPro: IPR000925; Glycoprot.G.  
DR Pfam: PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein. CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 1 37  
FT TRANSMEM 38 66  
FT DOMAIN 67 298  
FT DOMAIN 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 298 AA; 32586 MW; 993C3D2DD68BC634 CRC64;

Query Match 100.0%; Score 288; DB 1; Length 298;  
Best Local Similarity 100.0%; Pred. No. 6.9e-27;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197  
|||||

## RESULT 2

VGLG\_HRSV2  
ID VGLG\_HRSV2 STANDARD; PRT; 297 AA.  
AC P27021;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb642).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11252;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374005; PubMed=1895054;  
RA Cane P.A., Matthews D.A., Pringle C.R.;  
RT "Identification of variable domains of the attachment (G) protein of  
RT subgroup A respiratory syncytial viruses.";  
RL J. Gen. Virol. 72:2091-2096(1991).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
DR PIR; JQ1204; JQ1204.  
DR InterPro: IPR000925; Glycoprot.G.  
DR Pfam: PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37  
FT TRANSMEM 38 66  
FT DOMAIN 67 297  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32525 MW; 48448F9E091E1802 CRC64;

Query Match 99.0%; Score 285; DB 1; Length 297;  
Best Local Similarity 98.0%; Pred. No. 1.5e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197  
|||||

Query Match 99.0%; Score 285; DB 1; Length 297;  
Best Local Similarity 98.0%; Pred. No. 1.5e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197  
|||||

## RESULT 3

VGLG\_HRSV3  
ID VGLG\_HRSV3 STANDARD; PRT; 297 AA.  
AC P27022;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb1734).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11253;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374005; PubMed=1895054;  
RA Cane P.A., Matthews D.A., Pringle C.R.;  
RT "Identification of variable domains of the attachment (G) protein of  
RT subgroup A respiratory syncytial viruses.";  
RL J. Gen. Virol. 72:2091-2096(1991).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
DR PIR; JQ1205; JQ1205.  
DR InterPro: IPR000925; Glycoprot.G.  
DR Pfam: PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37  
FT TRANSMEM 38 66  
FT DOMAIN 67 297  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32525 MW; 48448F9E091E1802 CRC64;

Query Match 99.0%; Score 285; DB 1; Length 297;  
Best Local Similarity 98.0%; Pred. No. 1.5e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197  
|||||

## RESULT 4

VGLG\_HRSV6  
ID VGLG\_HRSV6 STANDARD; PRT; 297 AA.  
AC P27025;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb6256).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11256;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374005; PubMed=1895054;  
RA Cane P.A., Matthews D.A., Pringle C.R.;  
RT "Identification of variable domains of the attachment (G) protein of  
RT subgroup A respiratory syncytial viruses.";  
RL J. Gen. Virol. 72:2091-2096(1991).

Query Match 99.0%; Score 285; DB 1; Length 297;  
Best Local Similarity 98.0%; Pred. No. 1.5e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197  
|||||

Query Match 99.0%; Score 285; DB 1; Length 297;  
Best Local Similarity 98.0%; Pred. No. 1.5e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 KORQNKPPSKPNNDFFHFVFNVPVCSICSNNTPTCWAICKRIPNKKPGKK 197  
|||||

Query Match 99.0%; Score 285; DB 1; Length 297;  
Best Local Similarity 98.0%; Pred. No. 1.5e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;





DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb5857).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11254;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374005; PubMed=1895054;  
RA Cane P.A., Matthews D.A., Pringle C.R.;  
RT "Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";  
RL J. Gen. Virol. 72:2091-2096(1991).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
DR PIR; JQ1206; JQ1206.  
DR InterPro; IPR000925; Glycoprot\_G.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32772 MW; 10488CCA475936BE CRC64;  
Query Match 96.9%; Score 279; DB 1; Length 297;  
Best Local Similarity 95.9%; Pred. No. 7.8e-26;  
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KQKQKPPKPNNDHFEVFNPCISNNPTCWAICKRIPNKKPKK 49  
DB 149 KQKQKPPKPNNDHFEVFNPCISNNPTCWAICKRIPNKKPKK 197  
RESULT 8  
VGLG\_HRSV7  
ID VGLG\_HRSV7 STANDARD; PRT; 297 AA.  
AC P27026;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb6614).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11257;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374005; PubMed=1895054;  
RA Cane P.A., Matthews D.A., Pringle C.R.;  
RT "Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";  
RL J. Gen. Virol. 72:2091-2096(1991).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS

CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
DR PIR; JQ1209; JQ1209.  
DR InterPro; IPR000925; Glycoprot\_G.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32670 MW; 58B384028E437ACD CRC64;  
Query Match 94.8%; Score 273; DB 1; Length 297;  
Best Local Similarity 93.9%; Pred. No. 4e-25;  
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KQKQKPPKPNNDHFEVFNPCISNNPTCWAICKRIPNKKPKK 49  
DB 149 KQKQKPPKPNNDHFEVFNPCISNNPTCWAICKRIPNKKPKK 197  
RESULT 9  
VGLG\_HRSV1  
ID VGLG\_HRSV1 STANDARD; PRT; 292 AA.  
AC P20896;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Human respiratory syncytial virus (subgroup B / strain 18537).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11251;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87289657; PubMed=2441388;  
RA Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;  
RT "The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigenically related proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
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DR EMBL; M17213; AAA47412.1; -.  
DR PIR; B32703; MGN218.  
DR InterPro; IPR000925; Glycoprot\_G.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 292 AA; 32306 MW; BC8C59F69CA7AFC2 CRC64;



```
QY | 6 KPSPKPNDF-----HFEVNFVPCISNNPTCWAIC-----KRIPNKKP 46
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db | 145 KPPINPSGPPENHQQHNHNSQTLPPVPCSTCEGNCACLGLCIGLERAPSR 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 12
VGLG_BRSV2          STANDARD;          PRT;          263 AA.
AC O10685;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN Bovine respiratory syncytial virus (strain 220-60) (BRS).
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=82819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97288324; PubMed=9143302;
RA Furze J., Roberts S., Wertz G., Taylor G.;
RT "Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
RL Virology 231:48-58(1997).
CC -|- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.
CC -|- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -|- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
HRS VIRUS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Y11205; CAAT2089.1; -.
DR HSSP; P22261; IBRV.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 176 182 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 263 AA; 28964 MW; A630883D51ED02D5 CRC64;

Query Match 27.8%; Score 80; DB 1; Length 263;
Best Local Similarity 29.8%; Pred. No. 0.017;
Matches 14; Conservative 9; Mismatches 20; Indels 4; Gaps 1;

QY | 4 QNKPPSKPNDFHFEVNFVPCISNNPTCWAIC-----KRIPNKKP 46
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db | 152 ESNPPENHQQHNHNSQTLPPVPCSTCEGNCACSLCIGLERAPSR 198
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 13
VGLG_BRSVS          STANDARD;          PRT;          257 AA.
AC O10686;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
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GN Bovine respiratory syncytial virus (strain Snook) (BRS).
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=82824;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97288324; PubMed=9143302;
RA Furze J., Roberts S., Wertz G., Taylor G.;
RT "Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
RL Virology 231:48-58(1997).
CC -|- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTININATING ACTIVITIES.
CC -|- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -|- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
HRS VIRUS.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; Y08719; CAA65969.1; -.
DR HSSP; P22261; IBRV.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 257 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 176 182 BY SIMILARITY.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 257 AA; 28362 MW; 09BDE6874421E79B CRC64;

Query Match 26.9%; Score 77.5; DB 1; Length 257;
Best Local Similarity 30.8%; Pred. No. 0.032;
Matches 16; Conservative 8; Mismatches 19; Indels 9; Gaps 2;

QY | 6 KPSPKP-----NNDFFH--FEVNFVPCISNNPTCWAICKRIPNKKPKG 48
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db | 145 KPPINPSGPPENHQQHNHNSQTLPPVPCSTCEGNCACLGLCIGLERAPSR 196
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 14
VGLG_BRSVM          STANDARD;          PRT;          263 AA.
AC O10687;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN Bovine respiratory syncytial virus (strain Wbh) (BRS).
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=82825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97288324; PubMed=9143302;
RA Furze J., Roberts S., Wertz G., Taylor G.;
RT "Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
RL Virology 231:48-58(1997).
```

CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B  
CC HRS VIRUS.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; Y08717; CAA69967.1; -.  
DR HSP; P22261; IBRV.  
DR InterPro; IPR000925; Glycoprot\_G.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).  
FT DISULFID 173 186 BY SIMILARITY.  
FT CARBOHYD 176 182 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 263 AA; 29050 MW; 0D06AF7FCB46B858 CRC64;  
Query Match 26.9%; Score 77.5; DB 1; Length 263;  
Best Local Similarity 29.0%; Pred. No. 0.033;  
Matches 20; Conservative 5; Mismatches 19; Indels 25; Gaps 3;  
Qy 6 KPPSKP-----NNDFH--FEVFNVPSCISNNPTCWAIC-----KR 40  
Db 145 KPPINSPGNNPDHNNQTLPHVPCSTCEGNCACSLICQIGPERASSRAPTITLKK 204  
Qy 41 IPNKKPKKK 49  
Db 205 TPKPTTKK 213  
RESULT 15  
VGLG\_ORSVW  
ID VGLG\_ORSVW STANDARD; PRT; 263 AA.  
AC Q86695;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Major surface glycoprotein G (Attachment glycoprotein G).  
GN G.  
OS Ovine respiratory syncytial virus (strain WSU 83-1578) (ORSV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=79699;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94103788; PubMed=8277288;  
RA Mallipeddi S.K.; Samal S.K.;  
RT "Analysis of the ovine respiratory syncytial virus (RSV) G  
RT glycoprotein gene defines a subgroup of ungulate RSV.";  
RL J. Gen. Virol. 74:2787-2791(1993).  
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B  
CC HRS VIRUS.  
CC -----

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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; S67863; AAB29551.1; -.  
DR EMBL; S67862; AAB29551.1; JOINED.  
DR HSP; P22261; IBRV.  
DR InterPro; IPR000925; Glycoprot\_G.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).  
FT DISULFID 173 186 BY SIMILARITY.  
FT CARBOHYD 176 182 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 263 AA; 29225 MW; 81A649C6047B3B71 CRC64;  
Query Match 26.9%; Score 77.5; DB 1; Length 263;  
Best Local Similarity 25.8%; Pred. No. 0.033;  
Matches 17; Conservative 10; Mismatches 18; Indels 21; Gaps 2;  
Qy 4 QNKPPSPKPNDF-HFEVFNVPSCISNNPTCWAIC-----KRIP 42  
Db 151 QKSNPSETQDDYSDFIQLPYVPCNICEDGSACLSLCQDRSESLDKALTTTPKTKPKPMT 210  
Qy 43 NKKPKGK 48  
Db 211 TKKPTK 216  
Search completed: November 22, 2002, 14:25:58  
Job time : 12 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:24:12 ; Search time 29 Seconds  
(without alignments)  
348.149 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQKPPSPNNDHFVEF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	288	100.0	293	12	Q9YVB3	Q9YVB3 human respi
2	285	99.0	278	12	Q9Q6U1	Q9Q6U1 human respi
3	285	99.0	278	12	Q9Q6T7	Q9Q6T7 human respi
4	285	99.0	278	12	Q9Q6T4	Q9Q6T4 human respi
5	285	99.0	278	12	Q9Q6T3	Q9Q6T3 human respi
6	285	99.0	278	12	Q9Q6T0	Q9Q6T0 human respi
7	285	99.0	279	12	Q9Q6U0	Q9Q6U0 human respi
8	285	99.0	279	12	Q9Q6T9	Q9Q6T9 human respi
9	285	99.0	279	12	Q9Q6T8	Q9Q6T8 human respi
10	285	99.0	279	12	Q9Q6T5	Q9Q6T5 human respi
11	285	99.0	279	12	Q9Q6T2	Q9Q6T2 human respi
12	285	99.0	279	12	Q9Q6S9	Q9Q6S9 human respi
13	285	99.0	279	12	Q9Q6S7	Q9Q6S7 human respi
14	285	99.0	279	12	Q9Q6S6	Q9Q6S6 human respi
15	285	99.0	279	12	Q9Q6S0	Q9Q6S0 human respi
16	285	99.0	279	12	Q9Q6R9	Q9Q6R9 human respi

17	285	99.0	292	12	Q9YVB2	Q9YVB2 human respi
18	285	99.0	292	12	Q9YVB0	Q9YVB0 human respi
19	285	99.0	295	12	Q86356	Q86356 respiratory
20	285	99.0	295	12	Q86359	Q86359 respiratory
21	285	99.0	295	12	Q86360	Q86360 respiratory
22	285	99.0	297	12	Q82074	Q82074 human respi
23	285	99.0	297	12	Q82078	Q82078 human respi
24	285	99.0	297	12	Q82066	Q82066 human respi
25	285	99.0	297	12	Q82067	Q82067 human respi
26	285	99.0	297	12	Q82071	Q82071 human respi
27	285	99.0	297	12	Q82057	Q82057 human respi
28	285	99.0	297	12	Q82058	Q82058 human respi
29	285	99.0	297	12	Q9YVB5	Q9YVB5 human respi
30	285	99.0	298	12	Q82073	Q82073 human respi
31	285	99.0	298	12	Q82065	Q82065 human respi
32	285	99.0	298	12	Q82068	Q82068 human respi
33	285	99.0	298	12	Q82075	Q82075 respiratory
34	285	99.0	298	12	Q09634	Q09634 human respi
35	285	99.0	298	12	Q01929	Q01929 human respi
36	280	97.2	279	12	Q9Q6S8	Q9Q6S8 human respi
37	280	97.2	293	12	Q9YVB1	Q9YVB1 human respi
38	280	97.2	296	12	Q86358	Q86358 respiratory
39	280	97.2	297	12	Q91944	Q91944 human respi
40	280	97.2	298	12	Q82061	Q82061 human respi
41	280	97.2	298	12	Q82075	Q82075 human respi
42	280	97.2	298	12	Q82076	Q82076 human respi
43	280	97.2	298	12	Q82062	Q82062 human respi
44	280	97.2	298	12	Q82056	Q82056 human respi
45	280	97.2	298	12	Q82060	Q82060 human respi

#### ALIGNMENTS

#### RESULT 1

Q9YVB3 ID Q9YVB3 PRELIMINARY; PRT; 293 AA.  
AC Q9YVB3;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Attachment glycoprotein G (Fragment).  
OS Human respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_taxID=11250;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VV6973;  
RX MEDLINE=99022964; PubMed=9806017;  
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;  
RT "Antigenic and genetic diversity among the attachment proteins of  
RT group A respiratory syncytial viruses that have caused repeat  
RT infections in children.";  
RL J. Infect. Dis. 178:925-932(1998).  
DR EMBL; AF065407; AAD02943.1; -  
DR InterPro; IPR000925; Glycoprot G.  
DR InterPro; IPR003880; Ppantne.attach.  
DR InterPro; IPR002965; P\_rich\_extensn.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
DR PRINTS; PR01217; PRICHEXTENS.  
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 293 AA; 32125 MW; 17B5B43396A63CCF CRC64;

Query Match 100.0%; Score 288; DB 12; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.6e-31;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KORQKPPSPNNDHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 49  
Db 144 KORQKPPSPNNDHFVEFVPCISCSNNPTCWAICKRIPNKKPGKK 192





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DR EMBL: AF193313; AAF23736.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30443 MW; 8E2974F2E1AE15C9 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 278;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 KORQKPPKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 6
Q906T0 PRELIMINARY; PRT; 278 AA.
AC Q906T0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
DE Glycoprotein (Fragment).
GN G.
OS Human respiratory syncytial virus...
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=94191.
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193316; AAF23739.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30440 MW; 8D38997DEB9A6292 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 278;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQKPPKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 7
Q906U0 PRELIMINARY; PRT; 279 AA.
AC Q906U0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
DE Glycoprotein (Fragment).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
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RN SEQUENCE FROM N.A.
RC STRAIN=91242;
RX MEDLINE=20283719; PubMed=10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193306; AAF23729.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30544 MW; 6B270AAEB1CB3533 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQKPPKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 8
Q906T9 PRELIMINARY; PRT; 279 AA.
AC Q906T9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Glycoprotein (Fragment).
DE Glycoprotein (Fragment).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91399;
RX MEDLINE=20283719; PubMed=10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea.";
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193307; AAF23730.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Ppantne.attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein_G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30570 MW; AF6CF9C1D8F8A97C CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;
Best Local Similarity 98.0%; Pred. No. 3.8e-31;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQKPPKPNDFHFEVFNFCVCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 9
Q906T8 PRELIMINARY; PRT; 279 AA.
AC Q906T8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Glycoprotein (Fragment).  
GN G.  
OS Human respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11250;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=92011;  
RX MEDLINE=20283719; PubMed=10823752;  
RA Choi E.H., Lee H.J.;  
RT "Genetic diversity and molecular epidemiology of the G protein of  
RT subgroups A and B of respiratory syncytial virus isolated over 9  
RT consecutive epidemics in Korea.";  
RL J. Infect. Dis. 181:1547-1556(2000).  
DR EMBL; AF193308; AAF23731.1; -;  
DR InterPro; IPR000925; Glycoprot\_G.  
DR InterPro; IPR003880; Ppantne\_attach.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 279 AA; 30498 MW; 4E1CDF2F7E569E3A CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;  
Best Local Similarity 98.0%; Pred. No. 3.8e-31;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KORQKPPKPNDFHFEVFNPCISCSNPTCWAICKRIPNKKPGKK 49  
DB 130 KORQKPPKPNDFHFEVFNPCISCSNPTCWAICKRIPNKKPGKK 178

- RESULT 10  
QY 0906T5 PRELIMINARY; PRT; 279 AA.  
AC Q906T5;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Glycoprotein (Fragment).  
GN G.  
OS Human respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11250;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=92415;  
RX MEDLINE=20283719; PubMed=10823752;  
RA Choi E.H., Lee H.J.;  
RT "Genetic diversity and molecular epidemiology of the G protein of  
RT subgroups A and B of respiratory syncytial virus isolated over 9  
RT consecutive epidemics in Korea.";  
RL J. Infect. Dis. 181:1547-1556(2000).  
DR EMBL; AF193311; AAF23734.1; -;  
DR InterPro; IPR000925; Glycoprot\_G.  
DR InterPro; IPR003880; Ppantne\_attach.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 279 AA; 30442 MW; F53F5932FCE77E89 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;  
Best Local Similarity 98.0%; Pred. No. 3.8e-31;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KORQKPPKPNDFHFEVFNPCISCSNPTCWAICKRIPNKKPGKK 49  
DB 130 KORQKPPKPNDFHFEVFNPCISCSNPTCWAICKRIPNKKPGKK 178

RESULT 11  
QY 0906T2 PRELIMINARY; PRT; 279 AA.  
AC Q906T2;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Glycoprotein (Fragment).  
GN G.  
OS Human respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11250;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=93057;  
RX MEDLINE=20283719; PubMed=10823752;  
RA Choi E.H., Lee H.J.;  
RT "Genetic diversity and molecular epidemiology of the G protein of  
RT subgroups A and B of respiratory syncytial virus isolated over 9  
RT consecutive epidemics in Korea.";  
RL J. Infect. Dis. 181:1547-1556(2000).  
DR EMBL; AF193314; AAF23737.1; -;  
DR InterPro; IPR000925; Glycoprot\_G.  
DR InterPro; IPR003880; Ppantne\_attach.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 279 AA; 30547 MW; 86DFD42DC8AF500 CRC64;

Query Match 99.0%; Score 285; DB 12; Length 279;  
Best Local Similarity 98.0%; Pred. No. 3.8e-31;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KORQKPPKPNDFHFEVFNPCISCSNPTCWAICKRIPNKKPGKK 49  
DB 130 KORQKPPKPNDFHFEVFNPCISCSNPTCWAICKRIPNKKPGKK 178

RESULT 12  
QY 0906S9 PRELIMINARY; PRT; 279 AA.  
AC Q906S9;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Glycoprotein (Fragment).  
GN G.  
OS Human respiratory syncytial virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11250;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=95026;  
RX MEDLINE=20283719; PubMed=10823752;  
RA Choi E.H., Lee H.J.;  
RT "Genetic diversity and molecular epidemiology of the G protein of  
RT subgroups A and B of respiratory syncytial virus isolated over 9  
RT consecutive epidemics in Korea.";  
RL J. Infect. Dis. 181:1547-1556(2000).  
DR EMBL; AF193317; AAF23740.1; -;  
DR InterPro; IPR000925; Glycoprot\_G.  
DR InterPro; IPR003880; Ppantne\_attach.  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 279 AA; 30529 MW; AEC4D787983D472D CRC64;

Search completed: November 22, 2002, 14:26:33  
Job time : 29 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:26:37 ; Search time 11 Seconds  
(without alignments)  
69.765 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	21.5	37	10	US-09-030-619-181
2	56	19.4	37	9	US-10-044-359-28
3	54	18.8	57	9	US-10-044-359-20
4	53	18.4	58	9	US-10-044-359-18
5	51	17.7	36	9	US-10-044-359-27
6	51	17.7	325	9	US-10-033-245-11
7	51	17.7	325	9	US-10-033-223-11
8	51	17.7	325	12	US-10-033-246-11
9	51	17.7	325	12	US-10-033-301-11
10	51	17.7	325	12	US-10-033-326-11
11	50.5	17.5	35	10	US-09-864-761-48887
12	50	17.4	58	9	US-10-044-359-16
13	50	17.4	102	10	US-09-864-761-35081
14	50	17.4	1010	10	US-09-759-152-2
15	50	17.4	1024	10	US-09-879-257A-30
16	49.5	17.2	217	10	US-09-853-161-71
17	49.5	17.2	217	10	US-09-852-659A-71
18	49.5	17.2	322	10	US-09-726-643-72
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22	49.5	17.2	1940	9	US-10-016-283-34
23	49	17.0	74	10	US-09-989-903-18
24	48.5	16.8	185	10	US-09-854-864-11
25	48.5	16.8	271	10	US-09-864-761-37986
26	48.5	16.8	281	10	US-09-854-864-10
27	48.5	16.8	465	9	US-09-987-021-6
28	48.5	16.8	465	10	US-09-957-485-6
29	48.5	16.8	566	10	US-09-801-368-418
30	48	16.7	67	10	US-09-764-887-215
31	48	16.7	461	9	US-09-898-234-15
32	48	16.7	461	9	US-09-899-429A-25
33	48	16.7	461	10	US-09-889-422-15
34	48	16.7	712	10	US-09-888-615-69
35	47.5	16.5	87	10	US-09-764-869-949
36	47.5	16.5	449	10	US-09-801-574-84
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39	47.5	16.5	608	10	US-09-803-589-2
40	47.5	16.5	608	10	US-09-803-589-8
41	47.5	16.5	608	12	US-10-105-929-13
42	47.5	16.5	727	10	US-09-445-023A-1
43	47.5	16.5	835	10	US-09-801-574-22
44	47.5	16.5	967	12	US-10-105-929-2
45	47	16.3	60	10	US-09-864-761-40201

#### ALIGNMENTS

#### RESULT 1

US-09-030-619-181

; Sequence 181, Application US/09030619B

; Patent No. US20020035061A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Timothy J.

; APPLICANT: Taylor, Robert

; APPLICANT: Erfile, Douglas

; APPLICANT: Fraser, Janet R.

; APPLICANT: West, Michael H.P.

; APPLICANT: McNicol, Patricia J.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

; TITLE OF INVENTION: WITH ANTIBIOTICS

; FILE REFERENCE: 660081.406

; CURRENT APPLICATION NUMBER: US/09/030,619B

; NUMBER OF SEQ ID NOS: 232

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 181

; LENGTH: 37

; TYPE: PRT

; ORGANISM: Leiurus quin-questriatus hebraeus

; US-09-030-619-181

Query Match 21.5%; Score 62; DB 10; Length 37;

Best Local Similarity 38.1%; Pred. No. 0.18;

Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 28 CSNNPTCAICRIPNKKPGK 48

I : I I I I I I I I I I

Db 7 CTTSCKCVQCRHLNHTSRGK 27

#### RESULT 2

US-10-044-359-28

; Sequence 28, Application US/10044359

; Patent No. US20020160454A1

; GENERAL INFORMATION:

; APPLICANT: Herriman, Rafael

; APPLICANT: Wong, James F.

; APPLICANT: Lee, Jian-Ming

; CURRENT FILING DATE: 2002-01-11

SECRET

**TITLE OF INVENTION:** Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding Same

;	APPLICANT:	Ferrara,Napoleone	
;	APPLICANT:	Fong,Sherman	
;	APPLICANT:	Gao,Wei-Qiang	
;	APPLICANT:	Goddard,Audrey	
;	APPLICANT:	Gurney,Austin L.	
;	APPLICANT:	Pan,James	
;	APPLICANT:	Roy,Margaret Ann	
;	APPLICANT:	Stewart,Timothy A.	
;	APPLICANT:	Tumas,Daniel	
;	APPLICANT:	Watanabe,Colin K.	
;	APPLICANT:	Wood,William I.	
;	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic	
;	TITLE OF INVENTION:	Acids Encoding the Same	
;	FILE REFERENCE:	P2930R1C9	
;	CURRENT APPLICATION NUMBER:	US/10/033,223	
;	CURRENT FILING DATE:	2001-12-27	
;	PRIOR APPLICATION NUMBER:	60/095,325	
;	PRIOR FILING DATE:	1998-08-04	
;	PRIOR APPLICATION NUMBER:	60/112,851	
;	PRIOR FILING DATE:	1998-12-16	
;	PRIOR APPLICATION NUMBER:	60/113,145	
;	PRIOR FILING DATE:	1998-12-16	
;	PRIOR APPLICATION NUMBER:	60/113,511	
;	PRIOR FILING DATE:	1998-12-22	
;	PRIOR APPLICATION NUMBER:	60/115,558	
;	PRIOR FILING DATE:	1999-01-12	
;	PRIOR APPLICATION NUMBER:	60/115,565	
;	PRIOR FILING DATE:	1999-01-12	
;	PRIOR APPLICATION NUMBER:	60/115,733	
;	PRIOR FILING DATE:	1999-01-12	
;	PRIOR APPLICATION NUMBER:	60/119,341	
;	PRIOR FILING DATE:	1999-02-09	
;	PRIOR APPLICATION NUMBER:	60/119,537	
;	PRIOR FILING DATE:	1999-02-10	
;	PRIOR APPLICATION NUMBER:	60/119,965	
;	PRIOR FILING DATE:	1999-02-12	
;	PRIOR APPLICATION NUMBER:	60/162,506	
;	PRIOR FILING DATE:	1999-10-29	
;	PRIOR APPLICATION NUMBER:	60/170,262	
;	PRIOR FILING DATE:	1999-12-09	
;	PRIOR APPLICATION NUMBER:	60/187,202	
;	PRIOR FILING DATE:	2000-03-03	
;	PRIOR APPLICATION NUMBER:	PCT/US99/12252	
;	PRIOR FILING DATE:	1999-06-02	
;	PRIOR APPLICATION NUMBER:	PCT/US99/28634	
;	PRIOR FILING DATE:	1999-12-01	
;	PRIOR APPLICATION NUMBER:	PCT/US99/28551	
;	PRIOR FILING DATE:	1999-12-02	
;	PRIOR APPLICATION NUMBER:	PCT/US00/03565	
;	PRIOR FILING DATE:	2000-02-11	
;	PRIOR APPLICATION NUMBER:	PCT/US00/04414	
;	PRIOR FILING DATE:	2000-02-22	
;	PRIOR APPLICATION NUMBER:	PCT/US00/05841	
;	PRIOR FILING DATE:	2000 -03-02	
;	PRIOR APPLICATION NUMBER:	PCT/US00/08439	
;	PRIOR FILING DATE:	2000-03-30	
;	PRIOR APPLICATION NUMBER:	PCT/US00/14941	
;	PRIOR FILING DATE:	2000-05-30	
;	PRIOR APPLICATION NUMBER:	PCT/US00/15264	
;	PRIOR FILING DATE:	2000-06-02	
;	PRIOR APPLICATION NUMBER:	PCT/US00/32678	
;	PRIOR FILING DATE:	2000-12-01	
;	NUMBER OF SEQ ID NOS:	38	
;	SEQ ID NO 11		
;	LENGTH:	325	
;	TYPE:	PRT	
;	ORGANISM:	Homo sapiens	
;	IS-10-033-223-11		

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/ PRIOR APPLICATION NUMBER: PCT/US00/14941
/ PRIOR FILING DATE: 2000-05-30
/ PRIOR APPLICATION NUMBER: PCT/US00/15264
/ PRIOR FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: 2000-12-01
/ NUMBER OF SEQ ID NOS: 38
/ SEQ ID NO. 11
/ LENGTH: 325
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-033-223-11

Query Match          17.7%;      Score 51;      DB 9;      Length 325;
Best Local Similarity 50.0%;      Pred. No. 38;
Matches          9;      Conservative          1;      Mismatches          8;      Indels          0;      Gaps

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QY 25 CSICSNNPTCWAICKRIP 42  
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Db 270 CPICKGNPCFAETAVIP 287

## RESULT 8

US-10-033-246-11  
; Sequence 11, Application US/10033246  
; Patent No. US20020098505A1  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2930R1C12  
; CURRENT APPLICATION NUMBER: US/10/033,246  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: 60/095,325  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/112,851  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: 60/113,145  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: 60/113,511  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/115,558  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115,565  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115,733  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/119,341  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: 60/119,537  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/119,965  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: 60/162,506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170,262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/187,202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28634  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/US00/14941  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 11  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-246-11

Query Match 17.7%; Score 51; DB 12; Length 325;  
Best Local Similarity 50.0%; Pred No. 38;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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Db 270 CPICKGNPCFAETAVIP 287

## RESULT 9

US-10-033-301-11  
; Sequence 11, Application US/10033301  
; Patent No. US20020098506A1  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2930R1C6  
; CURRENT APPLICATION NUMBER: US/10/033,301  
; CURRENT FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/095,325  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/112,851  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: 60/113,145  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: 60/113,511  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/115,558  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115,565  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115,733  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/119,341  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: 60/119,537  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/119,965  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: 60/162,506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170,262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/187,202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28634  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US00/03565



; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/US00/14941  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 11  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-301-11

Query Match 17.7%; Score 51; DB 12; Length 325;  
Best Local Similarity 50.0%; Pred. No. 38;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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DB 270 CPICKNGPNCFAETA VIP 287

RESULT 10  
US-10-033-326-11  
; Sequence 11, Application US/10033326  
; Patent No. US20020098507A1  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2930RIC8  
; CURRENT APPLICATION NUMBER: US/10/033,326  
; CURRENT FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/095,325  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/112,851  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: 60/113,145  
; PRIOR FILING DATE: 1998-12-16  
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; PRIOR APPLICATION NUMBER: 60/115,558  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115,565  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115,733  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/119,341  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: 60/119,537  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/119,965  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: 60/162,506

; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170,262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/187,202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28634  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/28551  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/US00/14941  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 11  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-326-11

Query Match 17.7%; Score 51; DB 12; Length 325;  
Best Local Similarity 50.0%; Pred. No. 38;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 25 CSICSNPTCWAICKRIP 42  
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DB 270 CPICKNGPNCFAETA VIP 287

RESULT 11  
US-09-864-761-48887  
; Sequence 48887, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4887
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL17332.16
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EST_HUMAN HIT: BF220308.1, EVALUE 5.00e-11
; OTHER INFORMATION: SWISSPROT HIT: P36627, EVALUE 4.30e-01
US-09-864-761-48887

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RESULT 12
US/10044-359-16
; Sequence 16, Application US/10044359
; Patent No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Herzman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10044, 359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599, 416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140, 227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Hottentotta judaica
US/10044-359-16

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RESULT 13
US-09-864-761-35081
; Sequence 35081, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35081
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004897.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: SWISSPROT HIT: P14077, EVALUATE 1.00e-09
; OTHER INFORMATION: EST_HUMAN HIT: AAC68227.1, EVALUATE 1.00e-34
US-09-864-761-35081

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Best Local Similarity 30.0%; Pred. No. 15;  
Matches 12; Conservative 4; Mismatches 8; Indels 16; Gaps 3;  
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Db 60 QNRNPPPR-----PCPLCQGNH--WKVHCPR 84

RESULT 14  
US-09-759-152-2  
; Sequence 2, Application US/09759152  
; Patent No. US20020028433A1  
; GENERAL INFORMATION:  
; APPLICANT: Palmer, Michelle A.J.  
; APPLICANT: Gee, Melissa  
; APPLICANT: Tillotson, Bonnie  
; APPLICANT: Chang, Xiao-Jia  
; TITLE OF INVENTION: Systems for Sensitive Detection of G-Protein Coupled  
; TITLE OF INVENTION: Receptor and Orphan Receptor Function Using Reporter  
; FILE REFERENCE: 4085-235-27 CIP  
; CURRENT APPLICATION NUMBER: US/09/759,152  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 09/654,499  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: US 60/180,669  
; PRIOR FILING DATE: 2000-02-07  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1010  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: PICAST ALC.  
US-09-759-152-2

Query Match 17.4%; Score 50; DB 10; Length 1010;  
Best Local Similarity 38.7%; Pred. No. 1.7e+02;  
Matches 12; Conservative 3; Mismatches 10; Indels 6; Gaps 1;  
QY 10 KPNDHFHFVFNFPVPCSCSNNPTCWAICR 40  
Db 350 KONN-----FNAVRCSHYPNHPWLTCLDR 374

RESULT 15  
US-09-879-257A-30  
; Sequence 30, Application US/09879257A  
; Patent No. US20020081690A1  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, SACHIKO  
; APPLICANT: HANADA, TOSHIRO  
; APPLICANT: SHIRO, MINORO  
; APPLICANT: KOBATAKE, SHINZO  
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF  
; FILE REFERENCE: 55986(70281)  
; CURRENT APPLICATION NUMBER: US/09/879,257A  
; CURRENT FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 1024  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-879-257A-30

Query Match 17.4%; Score 50; DB 10; Length 1024;  
Best Local Similarity 38.7%; Pred. No. 1.7e+02;  
Matches 12; Conservative 3; Mismatches 10; Indels 6; Gaps 1;  
QY 10 KPNDHFHFVFNFPVPCSCSNNPTCWAICR 40  
Db 350 KONN-----FNAVRCSHYPNHPWLTCLDR 374

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:25:06 ; Search time 15 Seconds  
(without alignments)  
96.115 Million cell updates/sec

Title: US-09-202-035-1  
Perfect score: 288  
Sequence: 1 KORQKPPSKPNDHFHFEV.....NNPTCWAICKRIPNKKPGKK 49

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	288	100.0	681	6	Patent No. 5194595
2	285	99.0	298	2	Sequence 8, Appli
3	285	99.0	298	2	Sequence 8, Appli
4	285	99.0	298	3	Sequence 8, Appli
5	285	99.0	298	3	Sequence 8, Appli
6	285	99.0	298	4	Sequence 8, Appli
7	285	99.0	298	4	Sequence 8, Appli
8	285	99.0	298	4	Sequence 8, Appli
9	217	75.3	37	3	Sequence 12, Appli
10	193	67.0	32	3	Sequence 8, Appli
11	174	60.4	28	3	Sequence 4, Appli
12	151	52.4	37	3	Sequence 11, Appli
13	146	50.7	26	4	Sequence 9, Appli
14	145	50.3	30	4	Sequence 6, Appli
15	138	47.9	32	3	Sequence 7, Appli
16	134	46.5	23	4	Sequence 10, Appli
17	129	44.8	30	4	Sequence 5, Appli
18	125	43.4	28	3	Sequence 3, Appli
19	96	33.3	15	4	Sequence 53, Appli
20	96	33.3	16	3	Sequence 13, Appli
21	80	27.8	263	5	Sequence 13, Appli
22	66	22.9	32	3	Sequence 13, Appli
23	65	22.9	37	3	Sequence 10, Appli
24	65	22.6	28	3	Sequence 2, Appli
25	64	22.2	14	3	Sequence 9, Appli
26	64	22.2	14	4	Sequence 9, Appli
27	64	22.2	14	4	Sequence 9, Appli

28	64	22.2	17	3	US-08-721-979A-20	Sequence 20, Appl
29	64	22.2	17	4	US-08-836-501-20	Sequence 20, Appl
30	64	22.2	17	4	US-09-654-289-20	Sequence 20, Appl
31	64	22.2	28	3	US-08-793-792-1	Sequence 1, Appli
32	64	22.2	32	3	US-08-793-792-5	Sequence 5, Appli
33	64	22.2	37	3	US-08-793-792-9	Sequence 9, Appli
34	61	21.2	17	4	US-08-721-979A-19	Sequence 19, Appl
35	61	21.2	17	4	US-08-836-501-19	Sequence 19, Appl
36	61	21.2	17	4	US-09-654-289-19	Sequence 11, Appl
37	54	18.8	14	3	US-08-721-979A-11	Sequence 11, Appl
38	54	18.8	14	4	US-08-836-501-11	Sequence 11, Appl
39	54	18.8	14	4	US-09-654-289-11	Sequence 11, Appl
40	51	17.7	198	1	US-08-052-681-1	Sequence 1, Appli
41	50.5	17.5	115	2	US-08-540-406-8	Sequence 8, Appli
42	50.5	17.5	115	3	US-08-656-055-8	Sequence 8, Appli
43	50.5	17.5	115	4	US-08-954-668-8	Sequence 8, Appli
44	50.5	17.5	115	4	US-08-918-658-8	Sequence 8, Appli
45	50.5	17.5	115	5	PCT-US95-13233-8	Sequence 8, Appli

## ALIGNMENTS

RESULT 1  
5194595-19  
; Patent No. 5194595  
; APPLICANT: WATHEN, MICHAEL W.  
; TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING  
; IMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY  
; SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/543,780  
; FILING DATE: 31-OCT-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 137,387  
; FILING DATE: 23-DEC-1987  
; SEQ ID NO:19:  
; LENGTH: 681  
5194595-19

Query Match 100.0%; Score 288; DB 6; Length 681;  
Best Local Similarity 100.0%; Pred. No. 1.7e-26;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFHFEVFNPCISNNPTCWAICKRIPNKKPGKK 49  
DB 543 KORQKPPSKPNDHFHFEVFNPCISNNPTCWAICKRIPNKKPGKK 591

## RESULT 2

US-08-467-963C-8  
; Sequence 8, Application US/08467963C  
; Patent No. 5968776  
; GENERAL INFORMATION:  
; APPLICANT: KLEIN, Michel H  
; APPLICANT: DU, Run-Pan  
; APPLICANT: EWASYSHYN, Mary E  
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A  
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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Query Match          99.0%; Score 285; DB 2; Length 298;
Best Local Similarity 98.0%; Pred. No. 1.7e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: KLEIN, MICHEL H  
 ; APPLICANT: DU, Run-Pan  
 ; APPLICANT: EWASYSHYN, Mary E  
 ; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION  
 ; TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY  
 ; TITLE OF INVENTION: SYNCYTIAL VIRUS

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;
;
; TITLE OF INVENTION:  SYNCYTIAL VIRUS
;
; NUMBER OF SEQUENCES:  37
;
; CORRESPONDENCE ADDRESS:
;

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STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852.344D  
FILING DATE: 07-MAY-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,639  
FILING DATE: 14-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9200117.1  
FILING DATE: 06-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: STEWART, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-688 MIS:jfb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-852-344D-B

Query Match 99.0%; Score 285; DB 3; Length 298;  
Best Local Similarity 98.0%; Pred. No. 1.7e-26;

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Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKNNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
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Db 149 KORQKPPKNNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 197

RESULT 5
US-08-344-639E-8
; Sequence 8, Application US/08344639E
; Patent No. 6033668
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasyshyn, Mary E
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
; TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
; TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344.639E
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; CLASSIFICATION: 424
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-391 MIS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-639E-8

Query Match 99.0%; Score 285; DB 3; Length 298;
Best Local Similarity 98.0%; Pred. No. 1.7e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 149 KORQKPPKNNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 197

RESULT 6
US-08-467-969A-8
; Sequence 8, Application US/08467969A
; Patent No. 6168786
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasyshyn, Mary E
; TITLE OF INVENTION: CHIMERIC IMMUNOGENS
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
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; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasyshyn, Mary E
; TITLE OF INVENTION: Chimeric Immunogens
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,969A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; CLASSIFICATION: 435
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-475 MIS:bh
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-467-969A-8

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Best Local Similarity 98.0%; Pred. No. 1.7e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKNNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
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Db 149 KORQKPPKNNDFHFEVFPVCSICSNNTPTCWAICKRIPNKKPGKK 197

RESULT 7
US-08-467-961A-8
; Sequence 8, Application US/08467961A
; Patent No. 6171783
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasyshyn, Mary E
; TITLE OF INVENTION: Chimeric Immunogens
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
;
US-08-001-554A-8

Query Match          99.0%; Score 285; DB 4; Length 298;
Best Local Similarity 98.0%; Pred. No. 1.7e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKQKPPKPNDFHFEVFNFPVPCISCSNNPTCWAICKRIPNKKPGKK 49
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 9
US-08-793-792-12
; Sequence 12, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnostics
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,792
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
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US-08-793-792-12

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RESULT 10
US-08-793-792-8
; Sequence 8, Application US/08793792
; Patent No. 6077511
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnostics
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
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;; APPLICATION NUMBER: US/08/793,792  
;; FILING DATE:  
;; CLASSIFICATION: 514  
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;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-793-792-8

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US-08-793-792-4  
;; Sequence 4, Application US/08793792  
;; Patent No. 6077511  
;; GENERAL INFORMATION:

;; APPLICANT:  
;; TITLE OF INVENTION: Antigenic peptides derived from the  
;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
;; NUMBER OF SEQUENCES: 13  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/793,792  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-793-792-4

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 PNNDFHFEVFNVPSCSICNNPTCWAIC 28

RESULT 12  
US-08-793-792-11  
;; Sequence 11, Application US/08793792  
;; Patent No. 6077511  
;; GENERAL INFORMATION:

;; APPLICANT:  
;; TITLE OF INVENTION: Antigenic peptides derived from the  
;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
;; NUMBER OF SEQUENCES: 13

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/793,792  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 37 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-793-792-11

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Matches 25; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Db 2 KPKDDYHFEVFNVPSCICGNNQLCKSICKTIPSNK 37

RESULT 13  
US-08-750-624-9

;; Sequence 9, Application US/08750624  
;; Patent No. 6290971  
;; GENERAL INFORMATION:

;; APPLICANT: Kandil, Ali  
;; APPLICANT: James, Olive A  
;; APPLICANT: Chong, Pele  
;; APPLICANT: Klein, Michel H  
;; TITLE OF INVENTION: ADJUVANT COMPOSITIONS COMPRISING A  
;; TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND  
;; NUMBER OF SEQUENCES: 16  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sim & McBurney  
;; STREET: 6th Floor, 330 University Avenue  
;; CITY: Toronto  
;; STATE: Ontario  
;; COUNTRY: Canada  
;; ZIP: M5G 1R7

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/750,624  
;; FILING DATE: 26-FEB-1997  
;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stewart, Michael I  
;; REGISTRATION NUMBER: 24,973  
;; REFERENCE/DOCKET NUMBER: 1038-660  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (416) 595-1155  
;; TELEFAX: (416) 595-1163

;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 26 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-750-624-9

Query Match 50.7%; Score 146; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 4.4e-11;



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 14:16:41 ; Search time 35 Seconds  
(without alignments)  
186.551 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KQRQKPPKPNNDHFHFV.....NNPTCWAICKRIPNKKPGKK 49

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	288	100.0	49	AAW39217	Human RSV A subtyp
2	288	100.0	49	AAW39217	Human RSV A subtyp
3	288	100.0	49	AAW39248	Human RSV G protei
4	288	100.0	49	AAW39250	Human RSV G protei
5	288	100.0	49	AAW39251	Human RSV G protei
6	288	100.0	298	8 AAP70845	Sequence of human
7	288	100.0	298	13 AAR25302	HSRV glycoprotein
8	288	100.0	298	19 AAW47605	HRSV glycoprotein
9	288	100.0	298	23 AAU74676	Respiratory syncyt
10	288	100.0	681	10 AAP90441	Chimeric human res

11	285	99.0	49	19 AAW39218	Human RSV A subtyp
12	285	99.0	49	19 AAW39219	Human RSV A subtyp
13	285	99.0	49	19 AAW39221	Human RSV A subtyp
14	285	99.0	49	19 AAW39222	Human RSV A subtyp
15	285	99.0	49	19 AAW39223	Human RSV A subtyp
16	285	99.0	49	19 AAW39224	Human RSV A subtyp
17	285	99.0	59	17 AAR97073	Respiratory Syncyt
18	285	99.0	59	20 AAY44100	RSV G protein anti
19	285	99.0	59	22 AAB84145	Amino acid sequenc
20	285	99.0	61	17 AAR97072	Respiratory Syncyt
21	285	99.0	61	20 AAY44099	RSV G protein anti
22	285	99.0	61	22 AAB84144	Amino acid sequenc
23	285	99.0	101	16 AAR88253	RSV subgroup A wi
24	285	99.0	101	17 AAR95610	RSV sub-group A wi
25	285	99.0	101	17 AAR95616	Respiratory Syncyt
26	285	99.0	101	17 AAR97050	RSV G protein anti
27	285	99.0	101	20 AAY44078	A G2Na peptide der
28	285	99.0	101	21 AAB18805	Amino acid sequenc
29	285	99.0	101	22 AAG67741	Amino acid sequenc
30	285	99.0	101	22 AAB84123	Amino acid sequenc
31	285	99.0	101	22 AAB68016	Amino acid sequenc
32	285	99.0	101	22 AAB67775	Amino acid sequenc
33	285	99.0	232	20 AAR96314	Secreted G protein
34	285	99.0	298	14 AAR39286	Respiratory syncyt
35	285	99.0	298	20 AAR96313	Membrane bound G p
36	285	99.0	349	17 AAR95660	Streptococcal prot
37	285	99.0	349	22 AAB68028	Amino acid sequenc
38	285	99.0	452	22 AAB67771	Amino acid sequenc
39	283	98.3	49	19 AAW39220	Human RSV A subtyp
40	280	97.2	57	17 AAR97074	Respiratory Syncyt
41	280	97.2	57	20 AAY44101	RSV G protein anti
42	280	97.2	57	22 AAB84146	Amino acid sequenc
43	270	93.8	101	20 AAW97311	Peptide which indu
44	269	93.4	55	17 AAR97075	Respiratory Syncyt
45	269	93.4	55	20 AAY44102	RSV G protein anti

ALIGNMENTS

RESULT 1

AAW39217  
ID AAW39217 standard; peptide: 49 AA.

XX AAW39217;

XX 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A2.

XX G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.

XX Human respiratory syncytial virus.

XX Key Location/Qualifiers

FT Disulfide-bond 25..38

FT Disulfide-bond 28..34

XX W09746581-A1.

PD 11-DEC-1997.

XX 04-JUN-1997; 97WO-AU00351.

XX 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX

PT Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
PS  
XX Claim 5; Fig 2; 75pp; English.  
XX  
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to  
CC host cells and for characterisation of cell receptors for Pneumoviruses.  
CC When the fragments are used in combination with existing vaccines, they  
CC may allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;  
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e-28;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 KORQNKPPSKPNDFHFVFNVPSCSNNTCWAICKRIPNKKPGKK 49

RESULT 2  
AAW39244  
ID AAW39244 standard; peptide; 49 AA.  
AC AAW39244;  
XX  
XX 27-AUG-1998 (first entry)  
XX  
XX Human RSV G protein fragment (aa. 149-157) derivative #1.  
DE  
XX  
XX G protein; treatment; prevention; diagnosis; infection; immunity;  
KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
XX Human respiratory syncytial virus.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1 /note= "N-terminal acetylated"  
FT Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
FT Modified-site 49 /note= "C-terminal amide"  
FT  
XX WO9746581-A1.  
XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX  
XX WPI; 1998-042117/04.  
XX  
XX Peptide(s) derived from specific region of respiratory syncytial  
XX virus G protein - used to treat, prevent, diagnose and immunise  
XX against Pneumovirus infection  
XX  
XX Example 4; Fig 12; 75pp; English.  
XX  
XX AAW39244-W39252 are derivatives of the human respiratory syncytial virus  
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
XX can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,

CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to  
CC host cells and for characterisation of cell receptors for Pneumoviruses.  
CC When the fragments are used in combination with existing vaccines, they  
CC may allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;  
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e-28;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 KORQNKPPSKPNDFHFVFNVPSCSNNTCWAICKRIPNKKPGKK 49

RESULT 3  
AAW39248  
ID AAW39248 standard; peptide; 49 AA.  
XX  
XX AAW39248;  
AC  
XX 27-AUG-1998 (first entry)  
XX  
XX Human RSV G protein fragment (aa. 149-157) derivative #5.  
XX  
XX G protein; treatment; prevention; diagnosis; infection; immunity;  
KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
XX Human respiratory syncytial virus.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1 /note= "N-terminal fitc group"  
FT Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
FT Modified-site 49 /note= "C-terminal amide"  
FT  
XX WO9746581-A1.  
XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX  
XX WPI; 1998-042117/04.  
XX  
XX Peptide(s) derived from specific region of respiratory syncytial  
XX virus G protein - used to treat, prevent, diagnose and immunise  
XX against Pneumovirus infection  
XX  
XX Example 4; Fig 12; 75pp; English.  
XX  
XX AAW39244-W39252 are derivatives of the human respiratory syncytial virus  
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
XX can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
XX infection and to immunise against such infections. Antibodies raised  
XX from these fragments may also be used diagnostically. The fragments may  
XX also be used to identify compounds able to inhibit binding of RSV to  
XX host cells and for characterisation of cell receptors for Pneumoviruses.  
XX When the fragments are used in combination with existing vaccines, they  
XX may allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;  
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;  
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 Db 1 KORQNKPPSKPNDPFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49

## RESULT 4

AAW39250  
 ID AAW39250 standard; peptide; 49 AA.

XX AC AAW39250;

XX DT 27-AUG-1998 (first entry)

XX DE Human RSV G protein fragment (aa. 149-157) derivative #7.

XX KW G protein; treatment; prevention; diagnosis; infection; immunity;  
 XX antibody; Pneumovirus; identification; vaccine; cell receptor.

XX OS Human respiratory syncytial virus.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "N-terminal bb group"

XX FT Disulfide-bond 25..38

XX FT Disulfide-bond 28..34

XX FT Modified-site 49

XX FT /note= "C-terminal amide"

XX PN WO9746581-A1.

XX PD 11-DEC-1997.

XX PF 04-JUN-1997; 97WO-AU00351.

XX PR 05-JUN-1996; 96AU-0000265.

XX PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX PI Gorman JJ;

XX DR WPI; 1998-042117/04.

XX PT Peptide(s) derived from specific region of respiratory syncytial  
 virus G protein - used to treat, prevent, diagnose and immunise  
 against Pneumovirus infection

XX PS Example 4; Fig 12; 75pp; English.

XX CC AAW39244-W39252 are derivatives of the human respiratory syncytial virus  
 (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
 can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
 infection and to immunise against such infections. Antibodies raised  
 from these fragments may also be used diagnostically. The fragments may  
 also be used to identify compounds able to inhibit binding of RSV to  
 host cells and for characterisation of cell receptors for Pneumoviruses.  
 CC When the fragments are used in combination with existing vaccines, they  
 may allow a reduction in dose, and thus side effects, of the vaccine.

XX SQ Sequence 49 AA;

Query Match 100.0%; Score 288; DB 19; Length 49;

Best Local Similarity 100.0%; Pred. No. 2.2e-28;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQNKPPSKPNDPFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49  
 |||||

Db 1 KORQNKPPSKPNDPFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49

## RESULT 5

AAW39251  
 ID AAW39251 standard; peptide; 49 AA.

XX AC AAW39251;

XX DT 27-AUG-1998 (first entry)

XX DE Human RSV G protein fragment (aa. 149-157) derivative #8.

XX KW G protein; treatment; prevention; diagnosis; infection; immunity;  
 XX antibody; Pneumovirus; identification; vaccine; cell receptor.

XX OS Human respiratory syncytial virus.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "N-terminal biot group"

XX FT Disulfide-bond 25..38

XX FT Disulfide-bond 28..34

XX FT Modified-site 49

XX FT /note= "C-terminal amide"

XX PN WO9746581-A1.

XX PD 11-DEC-1997.

XX PF 04-JUN-1997; 97WO-AU00351.

XX PR 05-JUN-1996; 96AU-0000265.

XX PA (BIOM-) BIOMOLECULAR RES INST LTD.

XX PI Gorman JJ;

XX DR WPI; 1998-042117/04.

XX PT Peptide(s) derived from specific region of respiratory syncytial  
 virus G protein - used to treat, prevent, diagnose and immunise  
 against Pneumovirus infection

XX PS Example 4; Fig 12; 75pp; English.

XX CC AAW39244-W39252 are derivatives of the human respiratory syncytial virus  
 (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
 can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
 infection and to immunise against such infections. Antibodies raised  
 from these fragments may also be used diagnostically. The fragments may  
 also be used to identify compounds able to inhibit binding of RSV to  
 host cells and for characterisation of cell receptors for Pneumoviruses.  
 CC When the fragments are used in combination with existing vaccines, they  
 may allow a reduction in dose, and thus side effects, of the vaccine.

XX SQ Sequence 49 AA;

Query Match 100.0%; Score 288; DB 19; Length 49;

Best Local Similarity 100.0%; Pred. No. 2.2e-28;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQNKPPSKPNDPFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49  
 |||||

Db 1 KORQNKPPSKPNDPFHFVFNPCISCSNNPTCWAICKRIPNKKPGKK 49

## RESULT 6

AAP70845  
 ID AAP70845 standard; protein; 298 AA.

XX AC AAP70845;

XX DT 05-APR-1991 (first entry)

XX DE Sequence of human respiratory syncytial virus (HRSV) A2 strain



Query Match 100.0%; Score 288; DB 19; Length 298;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-27;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFHFEVFNFCVCSNNPTCWAICKRIPNKKPGKK 49  
 |||||  
 Db 149 KORQKPPSKPNDHFHFEVFNFCVCSNNPTCWAICKRIPNKKPGKK 197

RESULT 9  
 AAU74676

ID AAU74676 standard; Protein; 298 AA.

XX AC AAU74676;

XX DT 09-APR-2002 (first entry)

XX DE Respiratory syncytial virus G protein.

XX KW RSV; G protein; heavily glycosylated protein; antianaemic; antiviral;  
 XX KW vaccine; gene therapy; paramyxovirus; sendai virus; PMV;  
 XX KW antiviral chemotherapeutic compound; humoral response;  
 XX KW cellular immune response; hpiv; paediatric respiratory disease;  
 XX KW globulin gene transfer; sickle cell disease; beta-thalassaemia;  
 XX KW human immunodeficiency virus infection; HIV.

XX OS Human respiratory syncytial virus.

XX PN W0200192548-A2.

XX PD 06-DEC-2001.

XX PF 22-MAY-2001; 2001WO-US16610.

XX PR 01-JUN-2000; 2000US-208701P.

XX PA (SUUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX PI Portner A, Takimoto T;

XX DR WPI: 2002-130534/17.

XX DR N-PSDB; AAS21045.

XX PT Recombinant Sendai virus useful in vaccines to protect infection by  
 paramyxoviruses, comprises exogenous nucleic acid encoding  
 paramyxovirus protein or its antigenic fragment

XX PS Disclosure; Page 48; 57pp; English.

XX CC The invention relates to a recombinant Sendai virus comprising an  
 CC exogenous nucleic acid encoding a paramyxovirus (PMV) protein or its  
 CC antigenic fragment. The virus may be administered in combination  
 CC with an antiviral chemotherapeutic compound. Two or more viruses  
 CC expressing different PMV proteins may be co-administered. Compositions  
 CC comprising the virus are useful for eliciting a humoral and/or  
 CC cellular immune response to a PMV in a mammal, particularly a human.  
 CC Further a recombinant Sendai virus comprising an exogenous nucleic acid  
 CC encoding a second PMV protein is also administered and priming and/or  
 CC boosting humoral or cellular immune response comprises administering  
 CC one or more of a recombinant or isolated PMV protein or its antigenic  
 CC fragment, a DNA vaccine encoding the same, and a non-Sendai viral  
 CC vector encoding a PMV protein. The recombinant virus is useful as an  
 CC effective vaccine against hpiv or RSV (the major causes of paediatric  
 CC respiratory disease) and also to express any gene of  
 CC interest in target cells, providing a positive medical impact on  
 CC impaired cells. Wild-type globin gene transfer (i.e. gene therapy)  
 CC into stem cells effects a cure for sickle cell disease or beta-  
 CC thalassaemia. The recombinant virus may also prove effective in  
 CC conferring immunity to human immunodeficiency virus (HIV) infection.  
 CC The Sendai virus replicates at level that is high enough to  
 CC induce sufficient immunity, but does not cause any harm to human  
 CC recipient. The present sequence represents a respiratory syncytial  
 CC virus (RSV) G protein (heavily glycosylated protein), a PMV protein

CC suitable for expression by the recombinant virus of the invention.  
 XX SQ Sequence 298 AA;

Query Match 100.0%; Score 288; DB 23; Length 298;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-27;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFHFEVFNFCVCSNNPTCWAICKRIPNKKPGKK 49  
 |||||  
 Db 149 KORQKPPSKPNDHFHFEVFNFCVCSNNPTCWAICKRIPNKKPGKK 197

RESULT 10

AAP90441

ID AAP90441 standard; protein; 681 AA.

XX AC AAP90441;

XX DT 01-NOV-1989 (first entry)

XX DE Chimeric human respiratory syncytial virus glycoproteins F and G.

XX KW Chimeric polypeptide; human respiratory syncytial virus;

XX KW protein F; protein G; vaccine.

XX OS Human respiratory syncytial virus.

XX PN W08905823-A.

XX PD 29-JUN-1989.

XX PF 31-OCT-1988; 88WO-US03784.

XX PR 23-DEC-1987; 87US-0137387.

XX PA (UPJO ) UPJOHN CO.

XX PI Wathen M;

XX DR WPI: 1989-206593/28.

XX PT Chimeric human respiratory syncytial virus polypeptides(s)  
 PT - contg. immunogenic fragments from HRSV glycoproteins  
 PT F and G, for vaccine prodn.

XX PS Claim 3; page 47-48; 50pp; English.

XX CC Chimeric polypeptide contg. a signal sequence and one or more  
 CC immunogenic fragments from both human respiratory syncytial virus  
 CC glycoproteins F and G. Can be used in vaccines. Hosts are, eg  
 CC E. coli, Chinese hamster ovary cells, murine CI27 cells and  
 CC S. frugiperda.

XX SQ Sequence 681 AA;

Query Match 100.0%; Score 288; DB 10; Length 681;  
 Best Local Similarity 100.0%; Pred. NO. 3.2e-27;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDHFHFEVFNFCVCSNNPTCWAICKRIPNKKPGKK 49  
 |||||  
 Db 543 KORQKPPSKPNDHFHFEVFNFCVCSNNPTCWAICKRIPNKKPGKK 591

RESULT 11

AAW39218

ID AAW39218 standard; peptide; 49 AA.

XX AC AAW39218;

XX DT 27-AUG-1998 (first entry)

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DE Human RSV A subtype G protein fragment (aa 149-157) strain long A.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-Al.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
XX WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
PS Claim 5; Fig 2; 75pp; English.
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;
XX
Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQNKPPSKPNNDHFVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
DB 1 KORQNKPPSKPNNDHFVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
RESULT 12
AAW39219
ID AAW39219 standard; peptide: 49 AA.
XX
AC AAW39219;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A642.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-Al.
XX

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PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
XX WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
PS Claim 5; Fig 2; 75pp; English.
XX
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;
XX
Query Match 99.0%; Score 285; DB 19; Length 49;
Best Local Similarity 98.0%; Pred. No. 5.3e-28;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORQNKPPSKPNNDHFVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
DB 1 KORQNKPPSKPNNDHFVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
RESULT 13
AAW39221
ID AAW39221 standard; peptide: 49 AA.
XX
AC AAW39221;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A6256.
XX
KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX
PN WO9746581-Al.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97WO-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
PI Gorman JJ;
XX
XX WPI; 1998-042117/04.
XX
PT Peptide(s) derived from specific region of respiratory syncytial

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PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection

PS Claim 5; Fig 2; 75pp; English.

XX  
XX  
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to  
CC host cells and for characterisation of cell receptors for Pneumoviruses.  
CC When the fragments are used in combination with existing vaccines, they  
CC may allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;  
Best Local Similarity 98.0%; Pred. No. 5.3e-28;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQKPPSKPNNDPHEFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49

Db 1 KORQKPPSKPNNDPHEFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49

RESULT 14

AAW39222  
ID AAW39222 standard; peptide; 49 AA.

XX  
XX AC AAW39222;

XX  
XX DT 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A6190.

XX G protein; treatment; prevention; diagnosis; infection; immunity;  
XX antibody; Pneumovirus; identification; vaccine; cell receptor.

XX Human respiratory syncytial virus.

XX Key Location/Qualifiers  
XX Disulfide-bond 25..38  
XX Disulfide-bond 28..34

XX WO9746581-A1.

XX  
XX PD 11-DEC-1997.

XX PF 04-JUN-1997; 97WO-AU00351.

XX PR 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection

XX Claim 5; Fig 2; 75pp; English.

XX  
XX  
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to  
CC host cells and for characterisation of cell receptors for Pneumoviruses.  
CC When the fragments are used in combination with existing vaccines, they

CC may allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;  
Best Local Similarity 98.0%; Pred. No. 5.3e-28;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQKPPSKPNNDPHEFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49

Db 1 KORQKPPSKPNNDPHEFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49

RESULT 15

AAW39223  
ID AAW39223 standard; peptide; 49 AA.

XX  
XX AC AAW39223;

XX  
XX DT 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A5857.

XX G protein; treatment; prevention; diagnosis; infection; immunity;  
XX antibody; Pneumovirus; identification; vaccine; cell receptor.

XX Human respiratory syncytial virus.

XX Key Location/Qualifiers  
XX Disulfide-bond 25..38  
XX Disulfide-bond 28..34

XX WO9746581-A1.

XX  
XX PD 11-DEC-1997.

XX PF 04-JUN-1997; 97WO-AU00351.

XX PR 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection

XX Claim 5; Fig 2; 75pp; English.

XX  
XX  
CC AAW39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to  
CC host cells and for characterisation of cell receptors for Pneumoviruses.  
CC When the fragments are used in combination with existing vaccines, they  
CC may allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;  
Best Local Similarity 98.0%; Pred. No. 5.3e-28;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KORQKPPSKPNNDPHEFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49

Db 1 KORQKPPSKPNNDPHEFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49

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Job time : 36 secs